



## SEQUENCE LISTING

<110> PITTMAN, DEBRA D.

<120> COMPOSITIONS AND METHODS FOR TREATING RAGE-ASSOCIATED DISORDERS

<130> WYTH-P01-002

<140> 10/643,589

<141> 2003-08-18

<150> 60/404,205

<151> 2002-08-16

<160> 13

<170> PatentIn version 3.5

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<211> 2057

<212> DNA

<213> Mus sp.

<220>

<223> Murine Soluble RAGE\_FC

<400> 1

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<220>  
 <223> Murine Soluble RAGE\_FC

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Pro Leu Val Leu Ser Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Gln  
35 40 45

Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu  
50 55 60

Ser Pro Gln Gly Gly Pro Trp Asp Ser Val Ala Gln Ile Leu Pro Asn  
65 70 75 80

Gly Ser Leu Leu Leu Pro Ala Thr Gly Ile Val Asp Glu Gly Thr Phe  
85 90 95

Arg Cys Arg Ala Thr Asn Arg Arg Gly Lys Glu Val Lys Ser Asn Tyr  
100 105 110

Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp Pro  
115 120 125

Ala Ser Glu Leu Thr Ala Ser Val Pro Asn Lys Val Gly Thr Cys Val  
130 135 140

Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp Gly  
145 150 155 160

Lys Leu Leu Ile Pro Asp Gly Lys Glu Thr Leu Val Lys Glu Glu Thr  
165 170 175

Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Arg Ser Glu Leu Thr  
180 185 190

Val Ile Pro Thr Gln Gly Gly Thr Thr His Pro Thr Phe Ser Cys Ser  
195 200 205

Phe Ser Leu Gly Leu Pro Arg Arg Arg Pro Leu Asn Thr Ala Pro Ile  
210 215 220

Gln Leu Arg Val Arg Glu Pro Gly Pro Pro Glu Gly Ile Gln Leu Leu  
225 230 235 240

Val Glu Pro Glu Gly Gly Ile Val Ala Pro Gly Gly Thr Val Thr Leu  
245 250 255

Thr Cys Ala Ile Ser Ala Gln Pro Pro Pro Gln Val His Trp Ile Lys  
 260 265 270

Asp Gly Ala Pro Leu Pro Leu Ala Pro Ser Pro Val Leu Leu Leu Pro  
 275 280 285

Glu Val Gly His Ala Asp Glu Gly Thr Tyr Ser Cys Val Ala Thr His  
 290 295 300

Pro Ser His Gly Pro Gln Glu Ser Pro Pro Val Ser Ile Arg Val Thr  
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Glu Thr Gly Asp Glu Gly Pro Ala Glu Gly Ser Val Gly Glu Ser Gly  
 325 330 335

Leu Gly Thr Leu Ala Leu Ala  
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<212> DNA  
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<220>  
<223> Murine solTNFRII\_FC

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tgttagcactg accaggtgga gacccgcgcc tgcactaac acgagaaccg agtgtgtgct	360	
tgcgaagctg gcaggtactg cgccttggaaa acccattctg gcagctgtcg acagtgcatt	420	
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ggactccggg taaatgagct cagcacccac aaaactctca ggtccaaaga gacacccaca	1740
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 <212> PRT  
 <213> Mus sp.

<220>  
 <223> Murine solTNFRII\_FC

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Trp Ala Thr Gly His Thr Val Pro Ala Gln Val Val Leu Thr Pro Tyr  
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Lys Pro Glu Pro Gly Tyr Glu Cys Gln Ile Ser Gln Glu Tyr Tyr Asp  
 35 40 45

Arg Lys Ala Gln Met Cys Cys Ala Lys Cys Pro Pro Gly Gln Tyr Val  
 50 55 60

Lys His Phe Cys Asn Lys Thr Ser Asp Thr Val Cys Ala Asp Cys Glu  
 65 70 75 80

Ala Ser Met Tyr Thr Gln Val Trp Asn Gln Phe Arg Thr Cys Leu Ser  
 85 90 95

Cys Ser Ser Ser Cys Ser Thr Asp Gln Val Glu Thr Arg Ala Cys Thr  
 100 105 110

Lys Gln Gln Asn Arg Val Cys Ala Cys Glu Ala Gly Arg Tyr Cys Ala  
 115 120 125

Leu Lys Thr His Ser Gly Ser Cys Arg Gln Cys Met Arg Leu Ser Lys  
 130 135 140

Cys Gly Pro Gly Phe Gly Val Ala Ser Ser Arg Ala Pro Asn Gly Asn  
 145 150 155 160

Val Leu Cys Lys Ala Cys Ala Pro Gly Thr Phe Ser Asp Thr Thr Ser  
 165 170 175

Ser Thr Asp Val Cys Arg Pro His Arg Ile Cys Ser Ile Leu Ala Ile  
 180 185 190

Pro Gly Asn Ala Ser Thr Asp Ala Val Cys Ala Pro Glu Ser Pro Thr  
 195 200 205

Leu Ser Ala Ile Pro Arg Thr Leu Tyr Val Ser Gln Pro Glu Pro Thr  
 210 215 220

Arg Ser Gln Pro Leu Asp Gln Glu Pro Gly Pro Ser Gln Thr Pro Ser  
 225 230 235 240

Ile Leu Thr Ser Leu Gly Ser Thr Pro Ile Ile Glu Gln Ser Thr Lys  
 245 250 255

Gly Gly

<210> 5  
<211> 585  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
Human RAGE-LBE fused to an Fc element

<220>  
<221> MOD\_RES  
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<223> Any amino acid

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20 25 30

Pro Leu Val Leu Lys Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg  
35 40 45

Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu  
50 55 60

Ser Pro Gln Gly Gly Pro Trp Asp Ser Val Ala Arg Val Leu Pro  
65 70 75 80

Asn Gly Ser Leu Phe Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Ile  
85 90 95

Phe Arg Cys Gln Ala Asn Ile Asn Arg Asn Gly Lys Glu Thr Lys Ser  
100 105 110

Asn Tyr Arg Val Arg Val Tyr Gln Ile Pro Glu Lys Pro Glu Ile Val  
115 120 125

Asp Ser Ala Ser Glu Leu Thr Ala Gly Val Pro Asn Lys Val Gly Thr  
130 135 140

Cys Val Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu  
145 150 155 160

Asp Gly Lys Pro Leu Val Leu Asn Glu Lys Gly Val Ser Val Lys Glu  
165 170 175

Gln Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu  
180 185 190

Leu Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser  
195 200 205

Cys Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala  
210 215 220

Pro Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln  
225 230 235 240

Leu Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val  
245 250 255

Thr Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp  
260 265 270

Met Lys Asp Gly Val Pro Leu Pro Leu Pro Ser Pro Val Leu Ile  
275 280 285

Leu Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala  
290 295 300

Thr His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser  
305 310 315 320

Ile Ile Glu Pro Gly Glu Gly Pro Thr Ala Gly Ser Val Gly Gly  
325 330 335

Ser Gly Leu Gly Thr Leu Ala Leu Ala Cys Ala Gly Ser Gly Ser Gly  
340 345 350

Ser Gly Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys  
355 360 365

Pro Ala Pro Glu Ala Leu Gly Ala Pro Ser Val Phe Leu Phe Pro Asp  
370 375 380

Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys  
385 390 395 400

Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp  
405 410 415

Tyr Val Asp Gly Val Glu Xaa Gln Asn Ala Lys Thr Lys Pro Arg Glu  
420 425 430

Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu  
435 440 445

His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn  
450 455 460

Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly  
465 470 475 480

Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu  
485 490 495

Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr  
500 505 510

Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn  
515 520 525

Lys Cys Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe  
530 535 540

Leu Tyr Ser Lys Leu Thr Asp Lys Ser Arg Trp Gln Gln Gly Asn Val  
545 550 555 560

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln  
565 570 575

Lys Ser Leu Ser Leu Ser Pro Gly Lys  
580 585

<210> 6  
<211> 1761  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence: Synthetic  
Human RAGE-LBE fused to an Fc element

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 <211> 404  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> HUMAN RAGE

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Pro Leu Val Leu Lys Cys Lys Gly Ala Pro Lys Lys Pro Pro Gln Arg  
 35 40 45

Leu Glu Trp Lys Leu Asn Thr Gly Arg Thr Glu Ala Trp Lys Val Leu  
 50 55 60

Ser Pro Gln Gly Gly Pro Trp Asp Ser Val Ala Arg Val Leu Pro  
 65 70 75 80

Asn Gly Ser Leu Phe Leu Pro Ala Val Gly Ile Gln Asp Glu Gly Ile  
 85 90 95

Phe Arg Cys Gln Ala Met Asn Arg Asn Gly Lys Glu Thr Lys Ser Asn  
 100 105 110

Tyr Arg Val Arg Val Tyr Gln Ile Pro Gly Lys Pro Glu Ile Val Asp  
 115 120 125

Ser Ala Ser Glu Leu Thr Ala Gly Val Pro Asn Lys Val Gly Thr Cys  
 130 135 140

Val Ser Glu Gly Ser Tyr Pro Ala Gly Thr Leu Ser Trp His Leu Asp  
 145 150 155 160

Gly Lys Pro Leu Val Pro Asn Glu Lys Gly Val Ser Val Lys Glu Gln  
165 170 175

Thr Arg Arg His Pro Glu Thr Gly Leu Phe Thr Leu Gln Ser Glu Leu  
180 185 190

Met Val Thr Pro Ala Arg Gly Gly Asp Pro Arg Pro Thr Phe Ser Cys  
195 200 205

Ser Phe Ser Pro Gly Leu Pro Arg His Arg Ala Leu Arg Thr Ala Pro  
210 215 220

Ile Gln Pro Arg Val Trp Glu Pro Val Pro Leu Glu Glu Val Gln Leu  
225 230 235 240

Val Val Glu Pro Glu Gly Gly Ala Val Ala Pro Gly Gly Thr Val Thr  
245 250 255

Leu Thr Cys Glu Val Pro Ala Gln Pro Ser Pro Gln Ile His Trp Met  
260 265 270

Lys Asp Gly Val Pro Leu Pro Leu Pro Pro Ser Pro Val Leu Ile Leu  
275 280 285

Pro Glu Ile Gly Pro Gln Asp Gln Gly Thr Tyr Ser Cys Val Ala Thr  
290 295 300

His Ser Ser His Gly Pro Gln Glu Ser Arg Ala Val Ser Ile Ser Ile  
305 310 315 320

Ile Glu Pro Gly Glu Glu Gly Pro Thr Ala Gly Ser Val Gly Gly Ser  
325 330 335

Gly Leu Gly Thr Leu Ala Leu Ala Leu Gly Ile Leu Gly Gly Leu Gly  
340 345 350

Thr Ala Ala Leu Leu Ile Gly Val Ile Leu Trp Gln Arg Arg Gln Arg  
355 360 365

Arg Gly Glu Glu Arg Lys Ala Pro Glu Asn Gln Glu Glu Glu Glu Glu  
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Arg Ala Glu Leu Asn Gln Ser Glu Glu Pro Glu Ala Gly Glu Ser Ser  
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Thr Gly Gly Pro

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<211> 1436  
<212> DNA  
<213> Homo sapiens

<220>  
<223> HUMAN RAGE

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ggtgctgaag tgtaaggggg cccccaagaa accaccccaag cggctggaat ggaaactgaa	180	
cacaggccgg acagaagctt ggaaggtcct gtctccccag ggaggaggcc cctgggacag	240	
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cagctccctt ttcttttcc cttgaactgt tctggcctca gaccaactct ctcctgtata	1320
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tgatgattaa acacctgaca catctcaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa	1436

<210> 9  
<211> 40  
<212> PRT  
<213> Homo sapiens

<220>  
<223> N-Terminal Human RAGE Sequence

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	10
	15

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20	25
	30

Pro Leu Val Leu Lys Cys Lys Gly	
35	40

<210> 10  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

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<210> 11  
<211> 36  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 11	
agaggcagga tccacaattt ctggcttccc aggaat	36

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<210> 12
<211> 56
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

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<210> 13
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
      primer

<400> 13
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